

VARIABLE HEAVY DOMAIN

	10	20	30	40
2C4	EVQLQSGPELVKFTSVKISKAS	[GFTFDYTD]	WVKQS	*
574	EVQLVESGGGLVQPGGSLRLSCAAS	[GFTFDYTD]	WVROA	** *
hum III	EVQLVESGGGLVQPGGSLRLSCAAS	[GFTFSYAMS]	WVROA	** *

	50	a	60	70	80
2C4	HGKSIEMIG	[DVNPNSGGSIYNQREK]	KASLTVDSSRIYVM	*** *	***** *
574	PGKLEWVA	[DVNPNSGGSIYNQREK]	RFTLSVDRSKNTLYL	*****	*** *
hum III	PGKLEWVA	[VISGGGSIYADSVKG]	RFTISRDNSKNTLYL	*****	*** *

	abc	90	100ab	110
2C4	EIRSLTFEDTAVYYCAR	[NLGFSFYFDY]	WGQGTTLTVSS	*** **
574	QMSIRAEADTAVYYCAR	[NLGFSFYFDY]	WGQGTTLTVSS	*****
hum III	QMSIRAEADTAVYYCAR	[GRVGYSLYDY]	WGQGTTLTVSS	

FIG. 1

# Variable Light Domain

	10	20	30	40
2C4	DTVMTQSHKINSTVGDRVSTC	[KASQDWSIGVA]	WYQQR	*
	**	****	*	*
574	DIQMTQSPSSLSASVGDRVTTC	[KASQDWSIGVA]	WYQQR	*
		*	**	***
hum KI	DIQMTQSPSSLSASVGDRVTTC	[KASQDWSIGVA]	WYQQR	
	50	60	70	80
2C4	GQSPKLLIY [SASYRYT]	GVPRFTGSGGTDFTFTISVQA	*	*
	**	*	*	*
574	GKAPKLLIY [SASYRYT]	GVPSRFTGSGGTDFTLTISLQ		
		*	****	
hum KI	GKAPKLLIY [AASSLES]	GVPSRFTGSGGTDFTLTISLQ		
	90	100		
2C4	EDLAVYYC [QQYIYPT]	FGGKTKLEIKRT	*	*
	*	*	*	*
574	EDFATYYC [QQYIYPT]	FGGKTKLEIKRT		
	***	*		
hum KI	EDFATYYC [QQYNSLPWT]	FGGKTKLEIKRT		

FIG. 2

Maytansinoids  
(DM1)

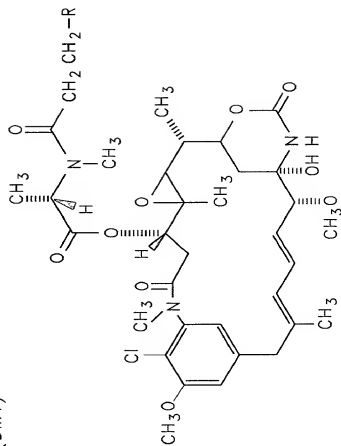
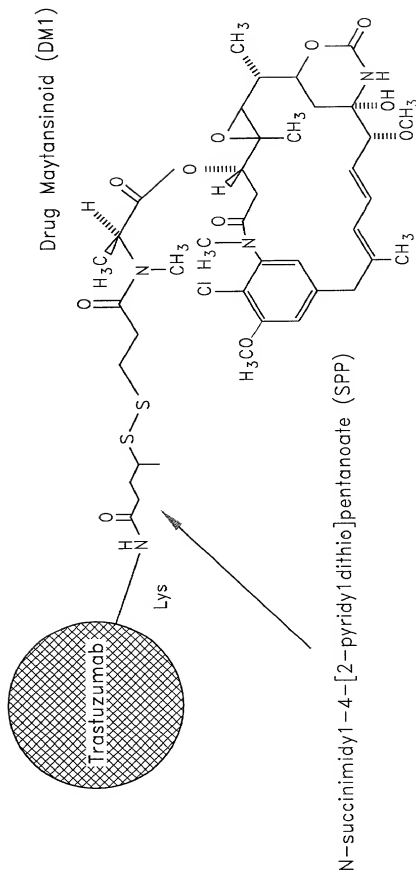


FIG. 3



**FIG. 4**

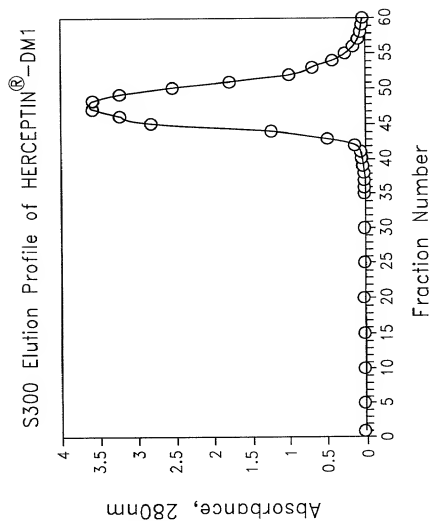


FIG. 5

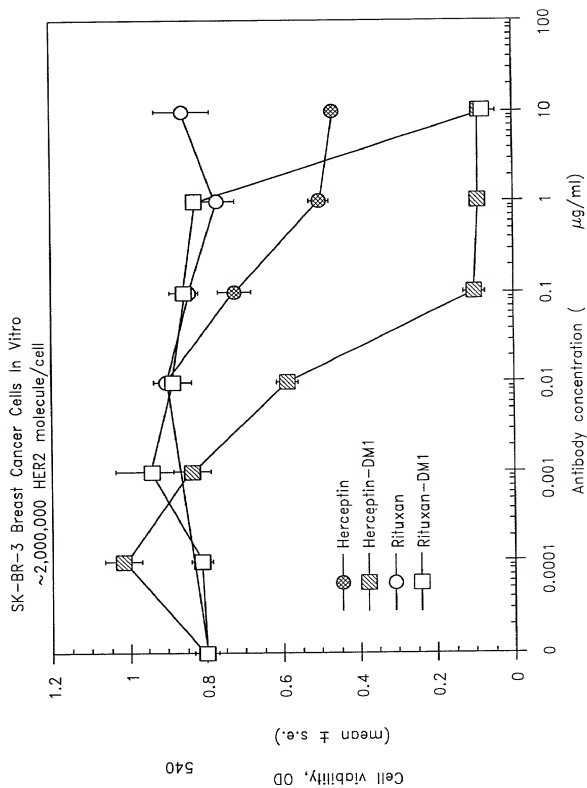


FIG. 6

[illegible][illegible][illegible]

FIG. 7A

[illegible]

FIG. 7B



[illegible]

•



501 CACCTATTGG TTTTACTGAC ATCCACTTTG CTTTCTCTTC CACAGGTGTC CTCCTCCACG TTCAATTACA GCTTTTACG GCGCGTAGC TTGATATCGA  
GTGGATAACC AGAATGACTG TAGTGTAAC GTAATGACAG GTGTCCACAG GTCTTAATGT CGAATTAATG CGGCGTAGCT AACATATAGCT  
^end of chimeric intron at pCI 989  
end of BS insert at hindIII^

601  
ATTCTCTGACG CCGGGGGGAT CCACATAGTG ATCCAAAGAA TTCAAAGAC CGCGCGCGG GCCCCACCC CTCGCACAC  
TAAGAGACGC GGGCCCCCTA GGTGATCAC TAGGTTCTT AGATTTCG AAGAATCCC GCGCGGGGC GCGGGGTGG GAGCGTCGTG GGGCGGGG  
\*end of BS intron insert at site

start of human HER2 from BS at xhol





301 GCTGCGACG CCTGTCTCC GATGTGTAG GGTCCCGCT GCTGGGGAGA GAGTCTGAG GATCTCAGA CCTGACGCG GATCTCTGT GCGGTGAGT  
CGACGCTGG GGACAGAGG CTACATTC CGAGGGCGA CGACCCCTCT CTCAGACTC CAGACGCT CGGACTGCG GTGACAGCA GGGCAGCGA  
191 A C H P C S P M C K G S R C W G E S S E D C Q S L T R T V C A G G C

301 GCTGCGACG CCTGTCTCC GATGTGTAG GGTCCCGCT GCTGGGGAGA GAGTCTGAG GATCTCAGA CCTGACGCG GATCTCTGT GCGGTGAGT  
CGACGCTGG GGACAGAGG CTACATTC CGAGGGCGA CGACCCCTCT CTCAGACTC CAGACGCT CGGACTGCG GTGACAGCA GGGCAGCGA  
191 A C H P C S P M C K G S R C W G E S S E D C Q S L T R T V C A G G C

FIG. 7H



xcmI                    sau3AI                    scrFI                    sau96I  
 scrFI                    mvaI                    avall  
 mvaI                    dpaII                    asuI  
 ecorII                    dpaI                    sandI  
 dsav                    bstNI                    ppuMI  
 bstNI                    fnu4HI/bsoFI                    nlaIV  
 bseKI                    bglII                    nlaIV  
 apyI                    mspI                    eco0109I/draII  
 nlaIV                    hpaII                    bsmFI                    mmlI                    tspRI                    tsprI  
 801 CAGTGCAGAT ATCCAGGAGT TTGCTGGTG CCAAGAGATC TTGCGAGGC TTGATGGGG ACCGAGCTC CACACTGCC  
 GTCACGGTTA TAGCTCTCA AACGACCGAC GTTCTTCTAG AAACCTCGG AGCCTTAAGA CGCCTCTCG TGGTTCGGAG GTTGTACGG  
 358 S A N I Q E F A G C K K I F G S L A F L P E S F D G D P A S N T A  
 bsmI                    aluI                    sau3AI                    mspI  
 bsmFI                    tseI                    mboI/ndeII                    hpaII                    haeIII/paII  
 dpaII                    pleI                    dpaII                    eaeI                    ddeI                    bpuAI  
 hinfI                    hinfI                    mboII                    maeII                    mmlI                    bbsI  
 bsmAI                    earI/bsp32I                    bstEII                    cfrI                    ddeI                    nmlI                    hgaI  
 901 CGCTCCAGC CAGACAGCT CCAAGTGTGT GAGATCTG AGAGATCMC AGGTACTTA TACATCTG CATTGGCCGA CAGCTGCT CACCTCAGG  
 GGCAGGTG GTCTGTGA GTTTCACAA CTCTGAGAC TTCTTAGT TCCATAGAT ATGTAGATC TCCCGGCT GTCCAGGA CTGAGTGC  
 391 P L Q P E Q L Q V E T L E E I T G Y L Y I S A W P D S L P D L S V  
 alwNI                    alw26I/bsmAI                    bsmFI                    hinPI                    hhaI/cfoI  
 bspMI                    bsaJI                    nciI                    nciI                    nari                    nari                    nari                    nari  
 mspI                    mspI                    hpaII                    hpaII                    hpaII                    hpaII                    hpaII                    hpaII  
 dsav                    dsav                    hglCI                    hglCI                    hglCI                    hglCI                    hglCI                    hglCI  
 001 TCTTCAGCA CTTGCAAGTA ATCCGGGGAC GAATTCGCA CAATGGCCG TACTGCTGA CCTTCAGG GCTGGCATC AGCTGGCTG GCTGGGCTC  
 AGAGGCTT GAGCTCAT TGGCCCTG GTTACAGCT GTTACCGG ATGAGCAT GGAAGTTC GGACCGTAG TCAGCCGACC CGAGCCGAG  
 425 F Q N L Q V I R G R I L H N G A Y S L T L Q G L G I S W L G L R S

FIG. 7J



sau96I

avaI

asuI

nlaIV

scrFI

mvaI

mwol

bspl286

bsmFI

bstAPI

bmyI

ecorII

hgiAI/aspHI

dsav

bspl286

nlaIV

bstNI

bsiHKA1

hgiCI

bsaKI

bmyI

banI

bsaI

apaLI/snoI

apvI

alv4II/snoI

bsaII

alul

nlaIV

acil

3

101

ACTGAGGGA

CTGGGCHG

GACTGGCCT

CATCCACAT

TACTGCTCT

GTGAGGGS

CCCTGGGACC

AGCTTTTC

GAACCCAC

458

TAATCTCCT

GAACCTGAC

CTGACCGGA

GTAGGTGTA

TTGTGGTGG

AGACAGACA

CTGTGGCC

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

sau96I

avaI

asuI

nlaIV

scrFI

mvaI

mwol

bspl286

bsmFI

bstAPI

bmyI

ecorII

hgiAI/aspHI

dsav

bspl286

nlaIV

bstNI

bsiHKA1

hgiCI

bsaKI

bmyI

banI

bsaI

apaLI/snoI

apvI

alv4II/snoI

bsaII

alul

nlaIV

acil

3

101

ACTGAGGGA

CTGGGCHG

GACTGGCCT

CATCCACAT

TACTGCTCT

GTGAGGGS

CCCTGGGACC

AGCTTTTC

GAACCCAC

458

TAATCTCCT

GAACCTGAC

CTGACCGGA

GTAGGTGTA

TTGTGGTGG

AGACAGACA

CTGTGGCC

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

sau96I

avaI

asuI

nlaIV

scrFI

mvaI

mwol

bspl286

bsmFI

bstAPI

bmyI

ecorII

hgiAI/aspHI

dsav

bspl286

nlaIV

bstNI

bsiHKA1

hgiCI

bsaKI

bmyI

banI

bsaI

apaLI/snoI

apvI

alv4II/snoI

bsaII

alul

nlaIV

acil

3

101

ACTGAGGGA

CTGGGCHG

GACTGGCCT

CATCCACAT

TACTGCTCT

GTGAGGGS

CCCTGGGACC

AGCTTTTC

GAACCCAC

458

TAATCTCCT

GAACCTGAC

CTGACCGGA

GTAGGTGTA

TTGTGGTGG

AGACAGACA

CTGTGGCC

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

sau96I

avaI

asuI

nlaIV

scrFI

mvaI

mwol

bspl286

bsmFI

bstAPI

bmyI

ecorII

hgiAI/aspHI

dsav

bspl286

nlaIV

bstNI

bsiHKA1

hgiCI

bsaKI

bmyI

banI

bsaI

apaLI/snoI

apvI

alv4II/snoI

bsaII

alul

nlaIV

acil

3

101

ACTGAGGGA

CTGGGCHG

GACTGGCCT

CATCCACAT

TACTGCTCT

GTGAGGGS

CCCTGGGACC

AGCTTTTC

GAACCCAC

458

TAATCTCCT

GAACCTGAC

CTGACCGGA

GTAGGTGTA

TTGTGGTGG

AGACAGACA

CTGTGGCC

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

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sau96I

avaI

asuI

nlaIV

scrFI

mvaI

mwol

bspl286

bsmFI

bstAPI

bmyI

ecorII

hgiAI/aspHI

dsav

bspl286

nlaIV

bstNI

bsiHKA1

hgiCI

bsaKI

bmyI

banI

bsaI

apaLI/snoI

apvI

alv4II/snoI

bsaII

alul

nlaIV

acil

3

101

ACTGAGGGA

CTGGGCHG

GACTGGCCT

CATCCACAT

TACTGCTCT

GTGAGGGS

CCCTGGGACC

AGCTTTTC

GAACCCAC

458

TAATCTCCT

GAACCTGAC

CTGACCGGA

GTAGGTGTA

TTGTGGTGG

AGACAGACA

CTGTGGCC

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

GGACCTCTG

sau96I

avaI

asuI

nlaIV

scrFI

mvaI

mwol

bspl286

bsmFI

bstAPI

bmyI

ecorII

hgiAI/aspHI

dsav

bspl286

nlaIV

bstNI

bsiHKA1

hgiCI

bsaKI

bmyI

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apaLI/snoI

apvI

alv4II/snoI

bsaII

alul

nlaIV

acil

301 GGCACCAACCA GTGTGTCAAC TCCCTTCGGG CAGAGGATG GFGAGGAAAT GCGAGTACT CGAGGGGCTC CCAGGGAGT ATGGAATG  
 CGGGTGGGT CACACAGTGT ACCTCGGTCA AGGAAGCCCC GCTCTCAG CACTCTCTTA CGCTCTAGA CGTCCCGAG CGTCCCTCA TACACTTACG  
 525 P T Q C V N C S Q F L R G Q E C V E C R V L Q G L P R E Y V N A  
  
 401 CAGGCACTT TGGCGTGG ACCCTGATG TCAGCCCGAG AATGCTCAG TGACTCTGTT TGGACCGAG CTTGACCAT GTGTGGCTG TGCCACTAT  
 GTCCGTGACA AACGGCAGG TGGGACTCAG AGTGGGGCTC TTACGATC ACTGACAAA AACTGGCTC CGACTGGTCA CACACCGAC ACGGTGATA  
 558 R H C L P C H P E C Q P Q N G S V T C F G P E A D Q C V A C A H Y  
  
 591 K D P P F C V A R C P S G V K P D L S Y M P I W K F P D E G A C Q

FIG. 7L

scfI  
 mveI  
 ecorII  
 dsav  
 bstNI  
 bssKI  
 apyI  
 sau96I  
 avaiI foki  
 asuI bstF5I  
 mslI  
 3601 AGCCTTGCCC CATCACTGCG ACCCACTCCT GTGTGACCT GGATGACAG GGTGCCCCG CCGAGCAGAG AGCAGACCT CTGACGTCCA TGCTCTGCG  
 TOGGAACGG GTAGTTGACG TGGGTGAGGA CACACTGGA CCTACTGTC CCGACGGGCG GCGTGTCTC TGCTGCGGA GACTGAGT AGCAGAGCG  
 625 P C P I N C T H S C V D L D D K G C P A E Q R A S P L T S I V S A  
 tseI  
 fnu4H/bsoFI  
 bbvI acII  
 cac8I malI  
 aatII bsmBI acII  
 ahalI/bsaHI  
 tail  
 maeII  
 hinII/acyI bsmAI  
 esp3I  
 mspl  
 mroI  
 bspMI  
 bspEI  
 bsaWI  
 sau3AI  
 mboI/ndeII  
 dpnII  
 dpmI  
 alwI  
 nlaIV  
 bstVI/xhoII  
 bamHI  
 alwI  
 mwOI  
 fnu4H/bsoFI hpaII tsaI  
 bbvI mboI accII csp6I sfaNI bsmAI bbvI  
 tseI  
 bstVI/xhoII  
 fnu4H/bsoFI hpaII tsaI  
 mwOI  
 bbvI mboI accII csp6I sfaNI bsmAI bbvI  
 3701 GGTGGTGGC ATTCTGTGG TGCTGTGTTT GGGGTGGTC TTGGGATCC TCATCAAGC AGCGAGCAG AGATCGGA AGTACAGT GCGGAGCTG  
 CCACCAAGC TAAGACGACC AGCAGAGAA CCCCCAGG AACCCTAGG AGTAGTGG TGCGTGGTC TTCTAGGCT TCAATGCTA CGCTCTGAC  
 658 V V G I L L V V L G V V F G I L I K R R Q Q K I R K Y T N R R L

FIG. 7M

691 L Q E T E L V E P L T P S G A M P N Q A Q M R I L K E T E L R K V R  
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FIG. 7N

[illegible]

[illegible]

FIG. 7P



[illegible]

FIG. 7R



[illegible]

FIG. 7S

[illegible]



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701 AGGACCTAGA GGAAGGCATC CAAACGCTGA TGGGAGGCT GGAAGATGC AGCCCCCGA CTGGCGGAT CTTCAGCAG ACCTACAGA AGTTGACAG
TCCTGGAICT CCTTCGGTAG GTTTCGACT ACCCTCCGA CCTCTACG TCGGGGCT GACCGCTA GAGTTGCT TGAAGTCT TCAAGCTGTG
^end of ex 4/ start ex 5

801 AAATCATAC AACGATGAG CACTACTCAA GAATCAGGG CTGCTTACT GCTTCAGGA GCATCGAC AGGTCGAGA CATTCCTGG CATCTGCAG
TTTGAGTGTG TTGCTACTGC GTGATGATT CTGATGCC GACGAGATG CGAGTCCT CTGTACTCT TTCACTCT GTAAGGACG GTAGCACTC

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FIG. 7V

[illegible]

FIG. 7W

[illegible]

```

scrFI
mvaI
ecorII
ecorII
dsvI
bstNI
bskI
apyI
haeIII/palI
mscI/palI
haeI
cfrI
hphI
301 GGGGTTTCAC CATATGGCC AGGTGTGCT COMACTCCTA ATCTCAGTG ATCTACCCAC CTGGCTCC GAATTTGCTG GATTACAGS GGTGAACCA
CCCCAAAGTG GTATAACGG TCCGACCAGA GGTGAGGAT TAGAGTCCAC TAGATGGTGS GAACCGAGS GTTTACGAC CCTAATGTCC GCACTTGGTG

sau3AI
mboI/ndeII
dpmI
hphI
bsaI
bmaI
301 GGGGTTTCAC CATATGGCC AGGTGTGCT COMACTCCTA ATCTCAGTG ATCTACCCAC CTGGCTCC GAATTTGCTG GATTACAGS GGTGAACCA
CCCCAAAGTG GTATAACGG TCCGACCAGA GGTGAGGAT TAGAGTCCAC TAGATGGTGS GAACCGAGS GTTTACGAC CCTAATGTCC GCACTTGGTG

haeI bstXI
styI haeIII/palI
bsaI mmlI tsp509I
301 GGGGTTTCAC CATATGGCC AGGTGTGCT COMACTCCTA ATCTCAGTG ATCTACCCAC CTGGCTCC GAATTTGCTG GATTACAGS GGTGAACCA
CCCCAAAGTG GTATAACGG TCCGACCAGA GGTGAGGAT TAGAGTCCAC TAGATGGTGS GAACCGAGS GTTTACGAC CCTAATGTCC GCACTTGGTG

mspI
cfr10I/bsrFI
bsaXI
styI sau96I hpaII
ncoI haeIII/palI
dssI asuI ageI
bsaI bfiXI
bspXI nlaIII bclI bmrI
301 TGGTCCCTTC CTGTCCTTC TGAATTAAA ARACTATAC CACGAGAGS AGCTCCAGC ACACATAGG CTACCTGCCA TGGCCGACCC GGTGGGACAT
ACAGAGAGS GACAGAGS ACTAATATIT ITTGTATG GTCTCTCTC TGGAGTCTG TGTGTATCC GATGACGGT ACCGGTTGS CCACCTGTA

hgiAI/aspHI
sau3AI
mboI/ndeII tru9I
dpmI bsp1286
dpmI bsiHKaI tsp509I
pvuI/bspCI mseI nlaIII
mcrI bmyI aseI/asnI/vspI
bsiEI apalI/snoI rcaI apoI
tsp509I alw44I/snoI bspHI tsp509I
301 TTGAGTGTGT TGTCTGAC TCCTCTCA TGGCTTGGT CCATCTAGTA GATGCTGT GAATTACGAT CGGTGCACAT TAATCATGA AATTCGTAAT
AACTCACGA ACAGACCGTG ACAGACCGA CGTGAATCA GGTGATCAT CTACGGACCA CTTAATGCTA GCCACGTGA ATTAACTACT TTAAGCATTA
^start of linker 2
^end of linker 2

```

FIG. 7Y

[illegible]

FIG. 72



[illegible]

001 GGCGTTTTTC CATAGGCTCC GCCCCCCTGA CGAGCATCAC AAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCGACAG GACTATAAAG ATACCAAGCG

bsaJf aluI mulI hnsI/cfoI fnuHf/bsfI actI haeII

201 AATGCTCAGC CTCTAGGTAT CTCAGTTCGG TGTAGTTCGT TCGCTCCAG CTGGGGCTGG TGCACGACC CCGCGTTTCAG CCGCGCCGCT CGCGCTTATC  
TTTACAGTGC GACATCCGAT GAGTTCAGCG ACATCCAGCA AGCGAGGTTT CAGCGCAGAC ACCTGCTTGG GGGGCAAGTC GGCGTGGCGA CGCGAAGAT  
scfi cdei alui alW41.shoi D5E1 mml/ctoi

FIG. 7AA



701 trn9I nlaIV  
 tsp509I hgiCI  
 trn9I mnlI  
 msei tspRI bani ddel  
 ahalII/draI maeII msei tsprI bani ddel  
 701 CTTTAAATTT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATAATGAGTA AACCTGGTCT GACATGTACC AATCGTTAAT CAGTAGGACA CCFATCTCAG  
 GAAATTTTAA TTTTACTTC AAAATTTAGT TAGAATTCAT ATATACTCAT TTGAACGACA CTGTCAATGG TTAGAATTA GTACTCCGT GGATAGAGTC  
 bsrI tseI  
 sau3AI fnu4HI/bsaFI  
 mboI/ndeI nlaIV bbvI  
 dpmII haeII/palI  
 foki bsrFI asuI tsprI bsrDI  
 dpmI abdI/eamII05I mnlI  
 801 CGATCTGCTC ATTCTGTTCA TCGATCTTG CCGTACTGCC CGTCTCTAG ATAACTACGA TACGGGAGGG CTTACCATCT GGCCCGAGTG CTGCAATGAT  
 CTAGACACGA TAAACACAGT AGGATACAC GACTAGAGG GCAGACAAATC TATTGTGCT ATGCCCTGCC GAACTGTAGA CGGGGTAC GACGTTACTA  
 bsmAI foki  
 bsaI  
 thal mspI bpaI/gsuI  
 fnuDII/mvnl mspI haeII/palI sau96I foki  
 bstUI hpaII mwoI hinpI maeII hpaII hnpI hnpI avaiI mnlI  
 acII hphI nlaIV cfrI0I/bsrFI cac8I hpaII asuI hhaI/cfoI asuI acII bstFI  
 901 ACCGGGAGAC CCACCTCTAC CCGCTCTCAGA TTTATCAGCA ATAAACAGC CAGCGGAGG GCGCGAGGC AGAAGTGSTC CTGCACATT ATCCGCTCC  
 TGGCGCTCTG GGTGGAGTG GCGGAGGTCT AAATAGTGT TATTGTGTC CGGCGCTTC CGGCTGGG TCTTCCAG GACGTTGAAA TAGGCGGAGG  
 scrFI  
 nciI talI  
 mspI hpaII  
 hpaII rnaI  
 tsp509I dsav rnaI  
 trn9I dsav maeI  
 msei bskI bfiI  
 bsrI asuI/asnI/vspI aluI  
 001 ATCCGAGTCA TTTATGTTTG CGGGAGGT AGAGTAAGTA GTTCGCCAGT TAAATGATTG CGCAACCTTG TTGCCATGTC TCGTGGCATC GTGGTGTAC  
 TAGGTGAGT AAATTAACAC GGCCTCTGA TCTCATCAT CAAAGCGTCA ACAGGTACG ACGACCGTGA CACACAGTG

FIG. 7CC

101 GTCGCTGTT TGTATGGCT TCATTACGT CGGTTTCCA ACATCAAGG CGAGTTACAT CATGCCCAT GTTGTGCANA AAAGCGTTA GCTCCTTCGG  
 CGAGCAGCA ACCATACCA AGTAAGTCA GGCACAGGT TGTAGTCC GTCATATGTA CTAGGGGTA CTAGCGTTT TTTCGCAT TTTCGCAT CGAGGAGCC

101 GTCGCTGTT TGTATGGCT TCATTACGT CGGTTTCCA ACATCAAGG CGAGTTACAT CATGCCCAT GTTGTGCANA AAAGCGTTA GCTCCTTCGG  
 CGAGCAGCA ACCATACCA AGTAAGTCA GGCACAGGT TGTAGTCC GTCATATGTA CTAGGGGTA CTAGCGTTT TTTCGCAT TTTCGCAT CGAGGAGCC

201 TCTTCGATC GTTGTACGAA GTAAATGTCG CGAGTGTGTA TCTCTCATGG TTTAGCAGC ACTGCATAT TCTCTTACTG TCATGCCATC CGTAGATGC  
 AGGAGGCTAG CACAGTCTT CATTCACCG GCGTCACAT AGTAGATACC ATATCGATC ATATCGATC TGTAGTATC AGAGATGC ATAGTATC GATTCATC

301 TTTTCTGTG GTGCTGATC CTCACCAAG TCATCTCGAG ATATGTTGAT GCGGCGACG AGTTGCTCT GCGGCGCTC ATCAGGAT AAATCGCGC  
 AAAAGACAT GACCACTCAT GAGTTGCTC AGTATGATC TTTATCATTA CCGCGCTGSC TCACAGGAA CCGGCGCGAG TAGTGCCCTA TTATGCGCG

401 CACATAGCAG AACCTTAAA GTGCTCATCA TTGGAACAG TTCTTCGGG GGAATATCT CAAGATCTT ACCCTGTG AGATCGCTT GATGTACG  
 GTGTATGTC TTGAATTTT CACGAGTAG AACCTTTTC AAGAGACCC GCTTTTGA GTTCTGAA TGGGACAC TGTAGTCAA GTCATATG

FIG. 7DD



```

scrFI
ncII
mspI
hpaII
dcaV
sfanI
fokI caulI
bstFI
aluI bskII drdI
901 ACAGCTTGTG TGTAAAGCGA TGCCGGGAGC AGACAGGCCG GTACAGGGCG GTTCGGGGGT GTTCGGGGGT AGCCATGACC CAGTCACGTA
TGTGACACAG ACAATCGCCT ACGGCCCTCG TCTGTTGGGG CAGTCCCGCG CAGTCGCCCA CACGCCCCA CAGCCCGCG TCGTACTGG GTACGTGCAAT

mmOI
hinPI
hhaI/cfoI
nlaIV
nari
kesI
hinII/acyI
hgiCI
haeII
sfanI eheI
mmOI bari
aciI ahaI/bsaHI
101 TACCGATACA GGGCCATTC GCCATTTCAG CTAACGCAACT GTTGGGAAGG GCGATCGGTS CGGGCTTTCT CGCTATTACG CCGACTGGCG AAGGGGGGT
ATGGCGTACT CCGCGTAAAG CGGTAAGTCC GATGGTGTG CAACGCTTCC CCGTAGCCAC GCGCGAGAA GCGATAATGC GGTCCAGCGC TTCCCCCTTA

mmOI
bstAPI
hgiAI/asphI
bspI286
bsiHKA1
sfanI
tru9I fnu4HI/bsaFI
msei
aciI
001 GCGATACCG AGTTGGCTTA ACTATGCGC ATCAGACGAG ATTGACTGA GAGTGCACCA TATGGCGTGT GAATACCGC ACAGATCGCT AAGGAGAAA
CGCTATCGC TCACCGAAT TGAATAGCGG TAGTCTGTC TACATGACT CTCACGTGCT ATACGCCACA CTTTATGGCG TGTCTACGCA TTCTCTTTT

mmOI
bstAPI
hgiAI/asphI
bspI286
bsiHKA1
sfanI
ddel bmyI ndel
rsal
asp6I
aciI alw4I/snoI
001 GCGATACCG AGTTGGCTTA ACTATGCGC ATCAGACGAG ATTGACTGA GAGTGCACCA TATGGCGTGT GAATACCGC ACAGATCGCT AAGGAGAAA
CGCTATCGC TCACCGAAT TGAATAGCGG TAGTCTGTC TACATGACT CTCACGTGCT ATACGCCACA CTTTATGGCG TGTCTACGCA TTCTCTTTT

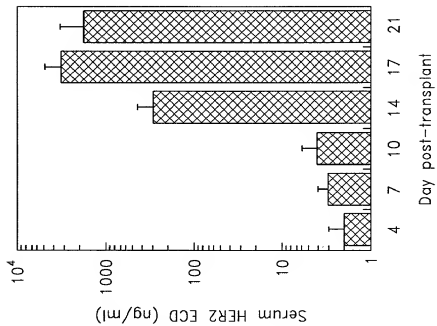
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mboI/ndeII
dpoII
qpcII haeIII/palI
pvuI/bspCI sau96I
mcrI asuI mboII
bsiEI cac8I earI/ksp62I
mmOI aciI mnlI
101 TACCGATACA GGGCCATTC GCCATTTCAG CTAACGCAACT GTTGGGAAGG GCGATCGGTS CGGGCTTTCT CGCTATTACG CCGACTGGCG AAGGGGGGT
ATGGCGTACT CCGCGTAAAG CGGTAAGTCC GATGGTGTG CAACGCTTCC CCGTAGCCAC GCGCGAGAA GCGATAATGC GGTCCAGCGC TTCCCCCTTA

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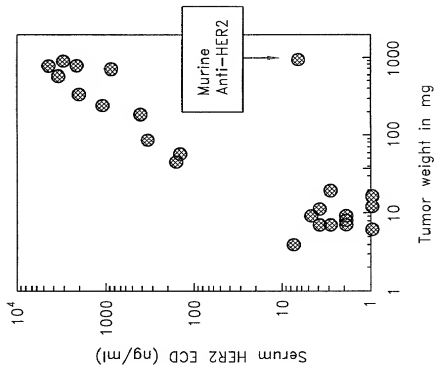
FIG. 7FF

[illegible]

**FIG. 7GG**



**FIG. 8A**



**FIG. 8B**



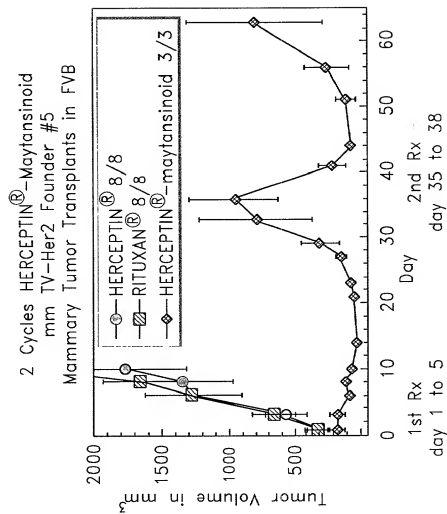


FIG. 9

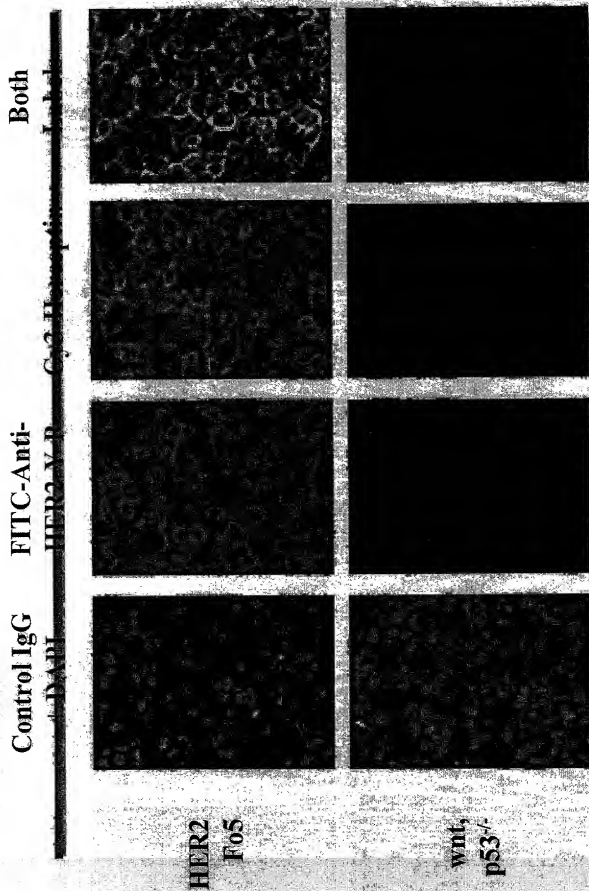


FIG. 10

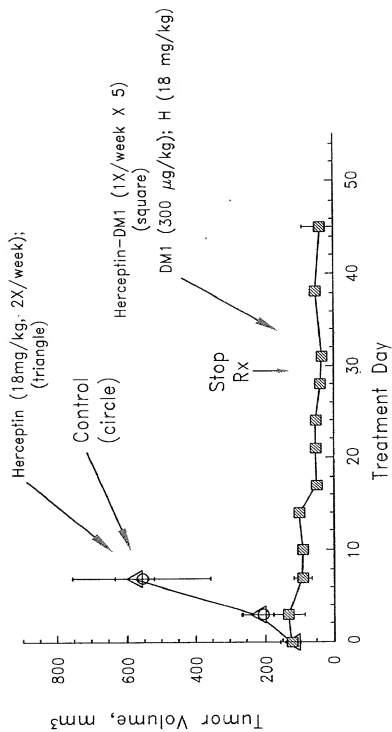


FIG. 11

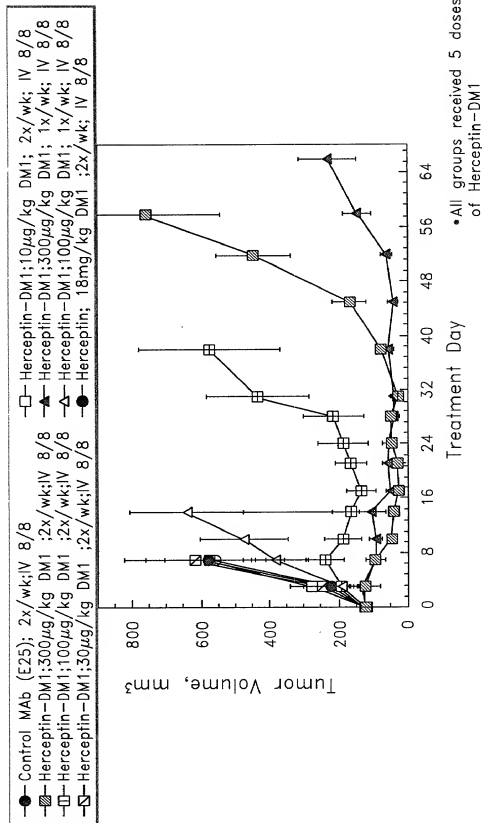


FIG. 12

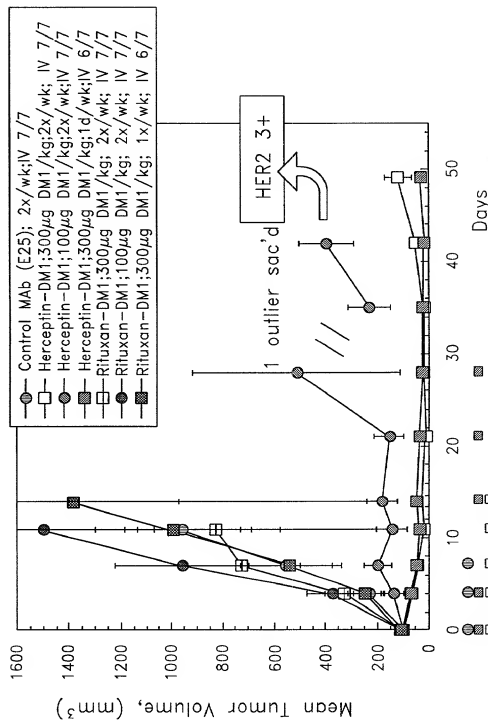


FIG. 13

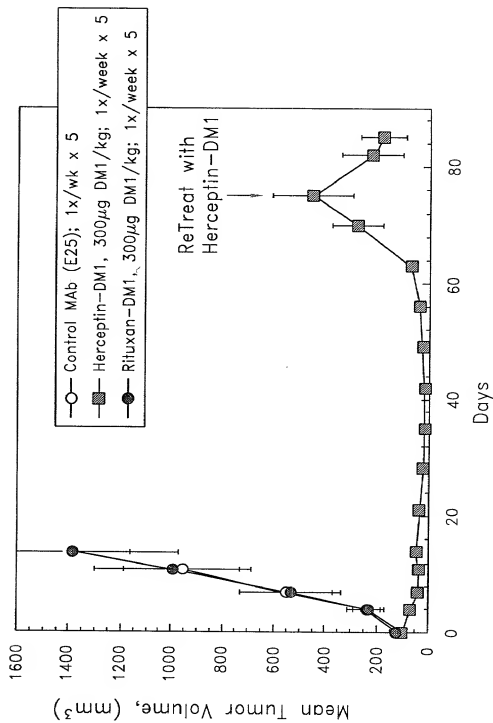


FIG. 14